

FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTGTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGC
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTGAGGGCCCCAGTATCAGG
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGATGTGTACC
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGATGAGGTTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTCAGGATTCCTGCTCTTTG
AAACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGCTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG
AACCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG
TGTTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAACTCTGAATTC
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEGKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFFSSVETNIGNFFDVMGTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHA VLK LAKGDEVWLRMGNGALHGDHQR FSTFAGFLLFETK

Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGCATGGCAAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT
GGGCCTGGCCCAGCCAGCCTCTGCCC GCCGGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTTC
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACC
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT
GGCCGGGCGGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCAC
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC
ACTCTGAGATATATAACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACTTCAGAGCTGCTCCTATCAGGTCCGT
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC
CACTGTGCCCTGGCACTGATTCTTCTCTTCTGCTTGCATAACTGATCATATTGCTTGTCTC
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT
TCTATACATAAAAGTTCCTACTTGTTAA

FIGURE 4

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLW
VTLTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFW
MDKVIELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFY
KKGKFSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI
LLELLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCC
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCA
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
CTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCT
GCGTGCTGCCCCGTTCAAGTTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGC
TCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACT
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

FIGURE 6

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKL
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAACATGCAGCTCGGCACTGGGCTCCTG
CTGGCCGCGCTCCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCACCAGTGCAC
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA
CTGCCACCCGGGTCCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCCCTACGTATCCATCGCTTGCTGCCAGAC
CAGCCTCTGCAACCATGACTGACGGCTGCCCTCCTCCAGGCCCGGACGCTCAGCCCCAC
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCCACC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCCTAGGGAAGTCCTGCGTGGAGTC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCTTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MQLGTGLLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCT
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG
CTGGGCTCGGGCGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTAGAGTC
GCGGGCTGCGCCCTGGGCAGAGGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCCGCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA
CAAAATGGCCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTG
ATGGAAGCAATTCACAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA
ATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC
CCTGCTCTTACTGATACTGGTTGCTTTTGAACCTGTTGTTTCCAGATGCTGCATAAAAGTA
AAGGAAGAACAACAACTAGTCCAAACCACTCTACACTGTGGATTTCAAAGAGTACCAGAAAA
GAAAGTGGCATGGAAGTATAAATAACTCATTTGACTTGGTTCCAGAATTTTGTAATTTCTGGAC
TGATAAGGAATGGCATCAGAACAACTAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAA
GATGAAGTGTAAGCTCCCCCTTAGAGCAAATATTAAGTAATTTTATATGTCTATTATTTTC
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC
CCAACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTTCATAAGTTGTTATCTA
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA
GTGTTTGATAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG
TACCATAGAAAAAGTTTGTCTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTC
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTTGTGCAAGACATGTGCCTTATAA
TTATTTTGTAGCTTAAAATTAAACAGATTTTGTAAATAATGTAACCTTTGTTAATAGGTGCATAA
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA
CACGTTGCCATATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC
TTGCCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC
ATTTTAGGAAGGAAAGGAACCTACGAAATCGTGTGAAATGGGTTGGAACCCATCAGTGATCG
CATATTCATTGATGAGGGTTTGTCTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC
TAGTTTCTTCAATGCTTACGCCTTGTTCCTTCTCAAGAGAAAGTTGTAACCTCTCTGGTCTTCA
TATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTCTTGTTCCTGGGGGAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACE
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKKNYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKS
RKTSTPNQSTLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGAATGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
CCACAGCCACTGGGCCCCAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC
GGTTCTCAGCCCCACACCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCCTGGTCTCAACGTCTATAGCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCTATGTTATGGGTCCATG
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGG
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTACGACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC
ACAGAGCCATCACACAGAGTGGGGTCTACACACCCAGGGATCATGACTCTCACCTTGGCCCTAGCTCAGA
AAATCGCAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTACGCAGAAAGAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCCTCATGGGTGTCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGGCTGGGGTCTCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
CAACACCCGTCTTGACCACTGTGGATGTGCCCCCTGAGATGATGCCACCGTCTATAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAAATGCCAGCGGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCACACCGTCA
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG
CGAAGATCAAACCTGCCTGGGTGAAGCCTGATCATGGGGCCGAGGGTGTCTTTGTGTTCCGGAGTCCCTTCTCA
TGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC
AGTGGACCACTTTGCCCCGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTAACCAGGCGG
AACAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG
AGACGTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAACAGGAAGGCCAGGAGGACCTCTGAGGCC
AGGCCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC
CCCCTGCTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA
ATGTCAACAAGCCGCTCCACCTCTGGGGCATTGTACAAGTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTCTCTAGCTTCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC
TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCCTAACCCCACTCTGTCAACCCACACAGGATCGGGTGGGA
CCTGGAGCTAGGGGGTGTGCTGAGTGAGTGAGTGAACACAGAAATATGGGAATGGCAGCTGTGAACCTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCTGAC
TAAGGCCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTGTCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTCACCAATTCAGCCCCCTGACCCTCAGGACGCTGGATG
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCCTCCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGCTATTGTACA
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTTCAAGTGAAGTGAGAG
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCTCCCTGCGCCTCTGCCTGGGCTCCCACTTTGGCA
GCACTTGAGGAGCCCTTAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGAGCCAGCT
CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG
AGTGAGTTCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG
GACCTGCAGCCCTCCATGCCTGACCCTCCCCCAACCCCGTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAG
CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGGGGTGACAGCGCGGGA
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
GGACTTGGAGAACCTTTATGTCTAGCTAAGGGATTGTAATAACACCGATGGGCACTCTGTATCTAGCTCAAGGTT
TGTAACACACCAATCAGCACCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT
ACTCTGGTGGGACTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT
TTGTGTCTAGCTCAGGGATCGTAACGCACCAATCAGCACCTGTCAAAACAGACCACTTGACTCTCTGTAAAAAT
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTCGGGTCCCCTCCCACGCGCTGGAAGCTTTGTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGKGTDRLVNVFLG
IPFAQPPLGPDRFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC
LVLNVYSPAIEVPAGSGRPVMVWHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFSGSAGGSIISGLVLSPPAAGLF
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVDGTVPFKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLA
ISTPVLTS L DVPPEMMPTVIDEYLG SNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLP SKIQQW
HQQQKNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAA
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCT
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG
ACAGAAATTACTTAGGGCTGAAGGAAGTGCACAAAAGAGTTTGGACCATCCCACTTCAGCGTG
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATC
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT
TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG
AGGATCTATGAGAAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG
GTCTCATTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
CAGTAGTGC GTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA
ATGAAGGATTTTTTTTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAG
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACT
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAAATGTAAATATATATACATAGATTCAAATCCTTATATAT
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTTTAAGTACAGGTTCCTAGTGTTTT
ACTATAACTGTCACATATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAAA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLELLQLKFLKPKINSFYAFEVKDAKGRTVSL
EKYKGKVS LVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFCNQFGESEPRPSKEVES
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP
IEVIRPDIAALVRQVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

TGTCGCCTGGCCCTCGCCATGCAGACCCCCGCGAGCGTCCCCCTCCCCGCCCCGGCCCTCCTGCTTCTGCTGCTGCTA
CTGGGGGGCGCCACGGCCTCTTTCCTGAGGAGCCGCGCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC
TATCCCGTGTTTTGTGGGCAGCGGGCCCGGACGCCTGACCCCCGAGAGGTGCTGACGACCTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGGATGAAG
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
GGTTCCAACGCCTTCAACCCGGTGTGCGCCAACCTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC
GGTATGGCCCGCTGCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT
ACTGTTACCGACTTCCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCGTG
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAAC
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCCGGCCCGTG
GTCTTCCCTGGGTTTTTTCCACGCCACGACATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG
GCAGCTGTGTTTTGAAGGCCGCTTCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG
GTGCTCGACCCCGGCCCGGTGCTGCGCAGCCCCCGGGATGAGTACAATGCCTCCAGCGCCTTGCCGGATGAC
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
CGGACCCTGATGAGGCACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCTGGGGCAACCAGACCGTT
GTCTTCCCTGGGTTCTGAGGCGGGGACGGTCTCAAGTTCTGTCGTCCGGCCCAATGCCAGCAGCTCAGGGACGTCT
GGGCTCAGTGTCTTCTGGAGGAGTTTGAACCTACCGGCCGGACAGGTGTGGACGCGCCGGCGGTGGCGAGACA
GGGACGCGGTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCGCTGCGTGGT
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC
GGGTGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCGGCCACAGAGCCGCCTTTGAGCAGGACGTGTCCGGG
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG
TCGGTGAACCTGCTGGTAACGTCGTGCGTGGCGGCCCTTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC
TGTTTCGTGGGCCTCCGTGAGCGCGGGAGCTGGCCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG
GGCGAGGCGGTGCTGAGCCTCAGCCGCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGCGGAGGCGGT
GGCGGTGGCGCGGGGTTCGCCCGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG
CTGAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCCGAGCAGACGCCGCTGCCGAGAAAGCGC
CTGCCACTCCGACCCGACCCCCACGCCCTGGGCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC
TCCGCTTCATCTCCTCCTGCTGCTGGCGCCCGCCGGGCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC
CCCGACGCGCCCTCTATGCTGCCCGGGCGCGCGCCTCCACGGCGACTTCCCGCTACCCCCCAGGCCAGC
CCGACCGCGCGGGTGGTGTCCGCGCCACGGGCCCCCTGGACCCAGCCTCAGCCCGCGATGGCCTCCCGCGG
CCCTGGAGCCCGCCCCGACGGGACGCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCTGCGC
CGCACCCACAGTTCAACAGCGGCGAGGCCCGGCCCTGGGACCGCCACCGCGGCTGCCACGCCCGGCCGGGACA
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCTAGCCGGGGGGCCCCCG
ATGCTTGGCAGTGCCAGCCACGGGAACAGGAGCGAGAGCGTGCCAGAACGCCGGGGCCGGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCGCGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAAACAG
CTCGCCCTCCCCCTACCCGGGGCGCAGGACGCTGAGACGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGCAGTTTTGGTTTCTTTTGGGTTTTCTAAC
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGACGGGAGGCTTGGACGCCGTGGGGAATGGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCCGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
TGGGCGTGTGTGTCAGTGGGCCACGCGTGCAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC
CCCCCCTCTGACAGGGAAGCGGGACAATGCCGGGTTTTCAGGACGAGACACGAGGAGGGCCTGCCCGGA
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA
ATACGGCCCCAGGTTGGTGAAGAGTCCCATGCCACCCGTCCCCCTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCTCCCCAGCCCCCTCCCCATCAAT
AAAACTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAGHLFPPEPPPLSVAPRDYLNHYPVFVGS GPGRLTPAEGA
DDLNIQVRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVC RMKGKQEG
ECRNFKVLLLRDESTLFVCGSNAFNPVCA^NYSIDTLQPVGDNISGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVVEWGSHVYFFFREI
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG
VVS LGGRPVLAVFSTPSNSIPGSAVCAFDLTQVA^NVFEGRFREQKSPESIWT^NFPVPEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTL^NMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ
RLLSLELDAASGGLLAAPRCVVRVPVARCQ^NYSGCMKNCIGSQDPYCGWAPD^NGSCIFLSPG
TRAAFEQDVSGASTSGLGDC^NTGLLRASLSEDRAGLVSVNLLVTSSVA^NAFVVGAVVSGFSVGW
FVGLRERRELARRKDKEAILAHGAGEAVLSVSR LGERRAQGPGRGGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLP
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPD^NRRRVVSAPTG
PLDPASAADGLPRPWSPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHL^NLPYGGADRTAPPVP

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC
AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTTCG
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC
ATTTATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTACATCTTCTCCAGGCGAAAAGGTCT
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGAC
CGAAAAGATGGGTCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAATCTGAAGGT
GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAGGGCCGGTTT
ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG
GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG
GGAAAGCAAAAATTCAGTGCCTGCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTTCATTTTTTTGATTTCTT
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACTTTTCCAGGAATAT
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC
TGAGGACGACCTCTTCCCTTGTAATTGCCATAGGAAAAAGACCAAAGATGAACTCTGATATG
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAGAAGAATT
TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA
TAAACACCTTTATTTTAAAGGAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF
TSSPGEKVFQVKVSAPEEQFTRVGVQVLDKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKS
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLDGWPLEKKKSNS
NIHPISWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK
IAKAGQEFARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA
GCCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCTCGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTTGTGTTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAA
AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGCGACGTCATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTAAATTATTCCCAAAGCATTGTGGAATATGATGGAACAAC
CTCATTTTTCTGTGTGAGATTACACAGAGGTGATAATAATGTCACGAGGCATTTGGATAAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCA**ATAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAACT
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT
CCCCTGTCTCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG
TTCACGTCAATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG
TGTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTGAGTGCCTCAGTTCTTGGAAGCT
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCC
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA
CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTG
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATC
CCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC
CCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPP
PLFSKVIVLIDALRDDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPHFVEYDGTTSFFVS
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAAC TGAC
AAATGCAACGCCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCTTGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
A TAGACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG
GAAAGGACAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGCTGT
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT
CCTTGGCAGGTTCTGGGTTTGGACGTTATTTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCG
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTT
CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
TGATCACGCGCCAGTATTTTCAGGACAAAGAACAGTCTTAAAAATATCAGAAAATACAGCTG
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT
TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCAGGCTCTGTATGAGACCCAGGC
TCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG
GAGTCAACGCGGAAGTATCCTATTCTTTTTTGATGCCTCAGAAAATATTCGAACGACCTTT
CAAATCAATCCTTTTTCTGGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCCTTCTGCAAGATGTAGGGTTT
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTCCAAC
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC
TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT
CTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAAT
AACGGTCTTGGTCTCCGACGTCAATGACAACGCCCCCGCCTTCACCCAAACCTCTACACCC
TGTTTCGTCCGCGAGAACAACAGCCCCGCCCCTGCACATCGGCAGCGTCAGCGCCACAGAGA
GACTCGGGCACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCAAGACCCGCACCTGCC
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCGCTGG
ACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCGCG
CTGAGCAGAGAGGCGCTGGTGC GCGTCTGGTGGTGGACGCCAACGACAACCTGCCCTTCGT
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAAGCCTGGCTG
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGGTGTGTGGGCGCACAATGGGGA
GGTGCGCACCCGAGGCTGCTGAGCGAGCGCGACGCAGCCAAGCACAGGCTCGTGGTGCTTG
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC
GGCTTCTCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGGCCAGGCCAGGCCGAGGC
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCCTCT
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG
TGCTCGGTGCCCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT
GTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCGGGACCAGTGAGTTCAAGT
TCTTGAAACCAGTTATTTTCGGATATTTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT
TCCACCTTCCGAAATAGCTTTGGATTAAATATTTCAGTAAAGTCTGTTTTTGTATTTTATATAC
TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTTCATCAT
TTTTTTGCATTAAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTTCTAAATGATAGTGT
AAGGTTTAAATTCTTTTCAACTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT
CTGAGGTTTTGATTTCATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTG
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT
CGTGTTTGAAAACCATGTCAATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC
CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGGCCAATATTTT
CTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGD
EGMIYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVLVDVNDNAPQFAQALYE
TQAPENSPIGFLIVKVAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQA MDGGGLSARCRVLVEVLD TNDNPPELIVSSFSNSVAENSPETPLAVFKIND
RDSENGKMCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTE
HNITVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDP
HLPLASLV SINADNGHLFALRSLDYEALQAFEFVVGATDRGSPALSREALVRVLVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDGSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAAQQA
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTK
GTVCIFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEI VHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
AAFFLEMAQLH

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**ATG**GGACCTGTGCGGTT
GGGAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAACTGAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTTT**TGA**CCCTTGCCTTTGAG
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTTCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAE LSRTGRSREVL
ELGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK
GLVQKGKVDLGIPLELWDEPSVEV TYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG
HVLPA AETACLQETWTGKEITDGE EKTEGEEEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTGTTTCCTGATTGTAACAACCTACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAAAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGAT**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274
><subunit 1 of 1, 223 aa, 1 stop
><MW: 25402, pI: 8.14, NX(S/T): 1
MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK
KGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAAGA
CCCTTTCTTGCCAGGTGCTGAGACAACCACACT**ATG**AGAGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAAACCCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT
TTTCGTCTACATTTTCTTAGTGTCAATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCTCTCAAGCTGGTGCTGTGTAG
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAGACCTTGTAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAG
ACCTTGTAACAATAAATAATTCTTGTGTAAAGTTAAATCATTTTTGTCCTAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACC**ATG**AGGACGCCTGGGCCTCTGCCCCTGCTGCTGCTG
CTCCTGGCGGGAGCCCCCGCCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG
ATGACTGCAATGCCTTGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA
GTTAGCAACCATGCTTCTCATTCCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC
AGACTTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC
ACATGGA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEY
IPVTTVLPDRQR

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA
GCCGCCAGTCCCGGCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTAC
TCCTCCTTTTCATTACATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA
AGCCGAGCGTGGAAGAATG GGGGTTCTCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAATAAAAC
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA
TTATGACTCTACTAAGAGTGGAATGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG
AGAAAACGATGAAACAGTATCTAACACATTAACTTGACAAATGGCTTGGAAGGAGAACTA
AACTTACAGTGAAGACAACCTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG
AAAAGTATTGATTGAGAAAAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT
CCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAT
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAACACTTC
TAATTCTGTGATTAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT
TAACCTTTTACAAGTGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIIQDGLAKGENDET
VSNTLTLTNGLERRTKTYSEDNFEELQYFPNIFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHKDKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

[illegible][illegible]

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLP
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY
RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCGATGTGGAGCGC
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGGCG
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSP
SNNQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACACAG
ACGTGAGCCACTCCACCCAGCCTAAACTTCATCTTCTTTGGATGAGATGAACACTTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT
CGTCATC**ATG**TCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTGGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAACTGGGAAT
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAACCAAAAAAAAAAAAAA

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAAG
CCCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCAC
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAG
ACTCATTTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT
CCCTTCCCCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT
ATACTCTGCTGTCCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCAGGCTCCCATATGTACCCCATCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN
LRCGTPEEPCQEAFNQTNRKLGITYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH
```

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA
GTCGGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT
ACCGCACCCAGGTTTCGGCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCC**AT**
GGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAAGTCTATAAGCTGTTTCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTT
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGC
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA
TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAGGAGACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTCATCACTTTCTCTTTAGAAAAAAGTACTACCTGTTAACAATTGGGAAAAG
GGGATATTCAAAAGTTCTGTGGTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA
TATTGCAGTTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAC
CTGTGATGCCCTAAGAAGCATTAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

FIGURE 46

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP
QLKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY
VLRGSCGLEYNLDYTELGQLKLGESGKHGFASFSDYYYKWSSADSCNMSGELITIVLLGIA
FVVYKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPPQNTGHGATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPL
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318